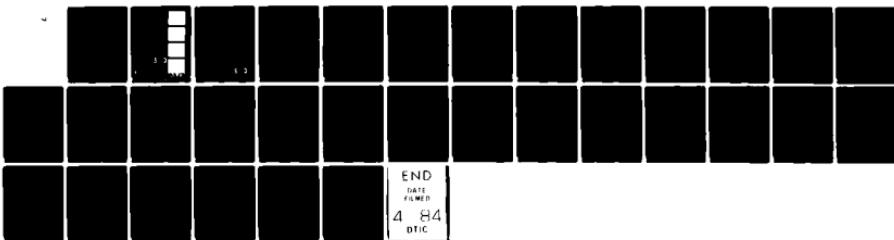


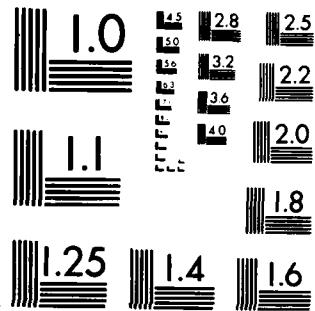
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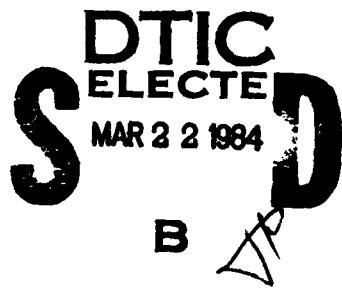
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Estimation of Latent Group Effects

Robert J. Mislevy

**Psychometric Technical
Report No. 2**

August 1983

This research was sponsored by the Personnel and Training Research Program, Psychological Sciences Division, Office of Naval Research under Contract No. N00014-83-0283, Contract Authority Identification No. NR 475-018, C

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| REPORT DOCUMENTATION PAGE | | READ INSTRUCTIONS BEFORE COMPLETING FORM |
|--|------------------------------------|--|
| 1. REPORT NUMBER Psychometric Technical Report No.2 | 2. GOVT ACCESSION NO. A1-R17271 | 3. RECIPIENT'S CATALOG NUMBER |
| 4. TITLE (and Subtitle) Estimation of Latent Group Effects | | 5. TYPE OF REPORT & PERIOD COVERED |
| | | 6. PERFORMING ORG. REPORT NUMBER |
| 7. AUTHOR(s) Robert J. Mislevy | | 8. CONTRACT OR GRANT NUMBER(s) N00014-83-C-0283 |
| 9. PERFORMING ORGANIZATION NAME AND ADDRESS NORC 6030 S. Ellis Avenue Chicago, IL 60637 | | 10. PROGRAM ELEMENT, PROJECT, TASK AREA & WORK UNIT NUMBERS 62763N RF63521803 RF63521 NR 475-018 |
| 11. CONTROLLING OFFICE NAME AND ADDRESS Personnel and Training Research Programs Office of Naval Research (Code 442PT) Arlington, VA 22217 | | 12. REPORT DATE August 1983 |
| | | 13. NUMBER OF PAGES 20 |
| 14. MONITORING AGENCY NAME & ADDRESS(if different from Controlling Office) | | 15. SECURITY CLASS. (of this report) Unclassified |
| | | 15a. DECLASSIFICATION/DOWNGRADING SCHEDULE |
| 16. DISTRIBUTION STATEMENT (of this Report) Approved for public release; distribution unlimited | | |
| 17. DISTRIBUTION STATEMENT (of the abstract entered in Block 20, if different from Report) | | |
| 18. SUPPLEMENTARY NOTES | | |
| 19. KEY WORDS (Continue on reverse side if necessary and identify by block number) | | |
| 20. ABSTRACT (Continue on reverse side if necessary and identify by block number) Conventional methods of multivariate normal analysis do not apply when the variables of interest are not observed directly, but must be inferred from fallible or incomplete data. For example, responses to mental test items may depend upon latent aptitude variables, which modeled in turn as functions of demographic effects in the population. A method of estimating such effects by means of marginal maximum likelihood, implemented by means of an EM algorithm, is proposed. Asymptotic standard errors, likelihood ratio tests of alternative | | |

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ESTIMATION OF LATENT GROUP EFFECTS

Robert J. Mislevy

**National Opinion Research Center
Chicago, Illinois**

AUGUST 1983

ESTIMATION OF LATENT GROUP EFFECTS

Abstract

Conventional methods of multivariate normal analysis do not apply when the variables of interest are not observed directly, but must be inferred from fallible or incomplete data. For example, responses to mental test items may depend upon latent aptitude variables, which modeled in turn as functions of demographic effects in the population. A method of estimating such effects by means of marginal maximum likelihood, implemented by means of an EM algorithm, is proposed. Asymptotic standard errors, likelihood ratio tests of alternative models, and computing approximations are provided. The procedures are illustrated with data for tests from the Armed Services Vocational Aptitude Battery administered to a national probability sample of American youth.

ESTIMATION OF LATENT GROUP EFFECTS

1. INTRODUCTION

Consider a number of multivariate normal populations in the random variable θ , with a common dispersion matrix and with means given by linear functions of the fixed group-effect parameters ζ . Consumer attitudes in the cells of a multi-way demographic design, for example, might be modeled in terms of only main effects and selected interactions. Maximum likelihood (ML) estimation of ζ from samples of θ from each population is well known, if it can be assumed that θ values are measured either without error or with iid normal and unbiased error components (Anderson, 1958).

Less familiar, however, are procedures to be followed when these assumptions are not tenable. If observations are of counts of favorable responses on an opinion survey, for example, the conditional distribution of observed score cannot be independent of expected score under any model with unbiased measurement errors (Lord and Novick, 1968:509). Or, as a second example, observed data may consist of subjects' responses to test items which depend stochastically on latent aptitude parameters through a quantal response model. More generally, we wish to consider situations in which it is not values of θ that are observed, but values of a secondary random variable x whose distributions depend on θ through known density functions $p(x|\theta)$.

This paper, then, presents a marginal maximum likelihood (MML) solution for ζ from x , along the lines employed by Bock and Aitkin (1981) to estimate parameters in item response models. The results extend those of Andersen and Madsen (1977) and Sanathanan and Blumenthal (1978), who estimate the mean and variance of a univariate normal latent distribution when $p(x|\theta)$ is the one-parameter logistic (Rasch) item response model, and of Andersen (1980), who tests the equality of latent means and variances in the same context.

We begin in Section 2 with a brief review of ML estimation of Γ and Σ , the common dispersion matrix, when values of $\tilde{\theta}$ are observed, or, in the terminology of Dempster, Laird, and Rubin (1977), the "complete data" problem. Section 3 considers the case in which values of x are observed instead, or the "incomplete data" problem. The resulting likelihood equations can be solved by means of cycles of an EM algorithm, which, since the unknown population density belongs to the exponential family, is guaranteed to converge to a local maximum. Computing approximations are presented in Section 4, asymptotic standard errors in Section 5, and likelihood ratio tests of fit in Section 6. Section 7 illustrates the procedures with data from the Profile of American Youth survey (U.S. Department of Defense, 1982).

2. THE "COMPLETE DATA" SOLUTION

We assume K homoscedastic p-variate normal distributions in the random variable $\tilde{\theta}$, with common dispersion matrix Σ and means μ_k given as linear functions of M fixed group-effect parameters γ_m ; that is,

$$\begin{bmatrix} \mu_1 \\ \vdots \\ \mu_M \end{bmatrix} = \begin{bmatrix} \gamma_1 \\ \vdots \\ \gamma_M \end{bmatrix} \begin{bmatrix} \gamma_1 \\ \vdots \\ \gamma_M \end{bmatrix}$$

or, more compactly,

$$\begin{matrix} \mu \\ K \times p \end{matrix} = \begin{matrix} T \\ K \times M \end{matrix} \begin{matrix} \gamma \\ M \times p \end{matrix}$$

where T is a known basis matrix, the k'th row of which specifies the dependence of μ_k on the parameters γ .

Suppose that samples of $\tilde{\theta}$ of size N_k have been obtained from the K populations. Let $N = \sum_k N_k$ and let I_{ik} be indicators that take the value 1 when observation i is associated with population k and 0 when it

is not. The likelihood of the sample is then given as

$$L = \prod_{i k} [g_k(\theta_i)]^{I_{ik}},$$

where

$$g_k(\theta_i) = \frac{|\Sigma|^{-1/2}}{(2\pi)^{p/2}} \exp[-\frac{1}{2}(\theta_i - \tilde{\Gamma}' \tilde{t}_k)' \Sigma^{-1} (\theta_i - \tilde{\Gamma}' \tilde{t}_k)].$$

For reference in a following section, we digress briefly to demonstrate that with population membership known, this density belongs to the exponential family. Considering its parameters to be $\tilde{\Gamma}$ and Σ^{-1} for convenience, we must show that it can be written in the form

$$f(\theta) = \exp \left\{ \sum_w A_w(\tilde{\Gamma}, \Sigma^{-1}) B_w(\theta) + C(\theta) + D(\tilde{\Gamma}, \Sigma^{-1}) \right\},$$

where the summation runs over the unique elements of $\tilde{\Gamma}$ and Σ^{-1} . Letting (σ^{uv}) represent Σ^{-1} , this can be done by taking

$$A_{uv}(\tilde{\Gamma}, \Sigma^{-1}) = \begin{cases} \sigma^{uv} & \text{if } u = v \\ 2\sigma^{uv} & \text{if } u \neq v \end{cases}$$

and

$$B_{uv}(\theta) = \theta_u \theta_v,$$

and for each element γ_{su} of $\tilde{\Gamma}$, taking

$$A_{\gamma_{su}}(\tilde{\Gamma}, \Sigma^{-1}) = \sum_v \sum_m \sigma^{uv} \gamma_{mv} \gamma_{su}$$

and

$$B_{\gamma_{su}}(\theta) = \sum_k \sum_m I_k t_{ks} t_{km} .$$

Finally,

$$C(\tilde{\Sigma}) = 0$$

and

$$D(\tilde{\Gamma}, \tilde{\Sigma}^{-1}) = \log^{-1}[|\tilde{\Sigma}|^{1/2} (2\pi)^{p/2}] .$$

Continuing to the main argument, we obtain the log likelihood as

$$\begin{aligned} \log L &= \sum_i \sum_k I_{ik} \log g_k(\theta_i) \\ &= C - N/2 \log |\tilde{\Sigma}| - \frac{1}{2} \sum_i \sum_k I_{ik} (\theta_i - \tilde{\Gamma}' \tilde{z}_k)' \tilde{\Sigma}^{-1} (\theta_i - \tilde{\Gamma}' \tilde{z}_k) \end{aligned} \quad (2.1)$$

where C does not depend on $\tilde{\Sigma}$ or $\tilde{\Gamma}$.

ML estimation proceeds by differentiating (2.1) with respect to $\tilde{\Gamma}$ and $\tilde{\Sigma}$, then equating the results to zero to obtain the likelihood equations:

$$\frac{\partial \log L}{\partial \tilde{\Gamma}} = \sum_i \sum_k I_{ik} \tilde{\Sigma}^{-1} (\theta_i - \tilde{\Gamma}' \tilde{z}_k) \tilde{z}_k' = 0$$

or

$$\sum_i \sum_k I_{ik} \theta_i \tilde{z}_k' = \sum_i \sum_k I_{ik} \tilde{\Gamma}' \tilde{z}_k \tilde{z}_k' ,$$

then

$$\sum_k N_k \hat{u}_k \tilde{z}_k' = \sum_k N_k \tilde{\Gamma}' \tilde{z}_k \tilde{z}_k' \quad (2.2)$$

where

$$\hat{u}_k = N_k^{-1} \sum_i I_{ik} \theta_i . \quad (2.3)$$

Rewriting (2.2) more compactly, we obtain the likelihood equation $\hat{\Sigma}$ as

$$\hat{T}' \hat{D} \hat{M} = \hat{T}' \hat{D} T \hat{\Gamma} ,$$

where

$$\hat{D} = \text{diag}(N_1, \dots, N_K) .$$

Assuming T to be of full column rank M (a condition which if not satisfied initially can always be met by reparameterizing in terms of contrast among the original χ 's), we obtain

$$\hat{\Gamma} = (\hat{T}' \hat{D} T)^{-1} \hat{T}' \hat{D} \hat{M} . \quad (2.4)$$

Likelihood equations for $\hat{\Sigma}$ are similarly obtained:

$$\begin{aligned} \frac{\partial \log L}{\partial \hat{\Sigma}} &= N/2(2 \hat{\Sigma}^{-1} - \text{diag } \hat{\Sigma}^{-1}) \\ &+ 1/2 \sum_i \sum_k I_{ik} \{ 2 \hat{\Sigma}^{-1} (\hat{\theta}_i - \hat{\Gamma}' \hat{t}_k) (\hat{\theta}_i - \hat{\Gamma}' \hat{t}_k)' \hat{\Sigma}^{-1} \\ &- \text{diag} [\hat{\Sigma}^{-1} (\hat{\theta}_i - \hat{\Gamma}' \hat{t}_k) (\hat{\theta}_i - \hat{\Gamma}' \hat{t}_k)' \hat{\Sigma}^{-1}] \} ; \end{aligned}$$

equating to zero and simplifying yields

$$\text{diag } \hat{\Sigma} - 2 \hat{\Sigma} = \text{diag } S - 2S \quad (2.5)$$

where

$$S = N^{-1} \sum_i \sum_k I_{ik} (\hat{\theta}_i - \hat{\Gamma}' \hat{t}_k) (\hat{\theta}_i - \hat{\Gamma}' \hat{t}_k)' . \quad (2.6)$$

After replacing $\hat{\Gamma}$ by $\hat{\Sigma}$, we see from the form of (2.5) that

$$\hat{\Sigma} = S . \quad (2.7)$$

It is well known that $\hat{\Gamma}$ and $\hat{\Sigma}$ are the unique zeros of the likelihood equations, and that they maximize the log likelihood function (2.1).

Note that (2.4) and (2.7) imply that \underline{M} and \underline{S} are jointly sufficient statistics for Γ and Σ . In anticipation of the incomplete data problem, it is instructive to recognize their computation in (2.3) and (2.6) as standard formulas for means and dispersions, Stieltjes integrals over not the unknown true density but over an approximation of it, namely, the discrete distribution given by a finite sample of points from the distribution of interest.

3. THE "INCOMPLETE DATA" SOLUTION

Suppose that rather than values of θ , we observe values of \underline{x} which depend on θ through $p(\underline{x}|\theta)$, densities of known form which may vary from one observation to the next. For example, \underline{x} you may be a vector of discrete values depending on the continuous latent variable θ through a quantal response model; or, as a second example, \underline{x} may be equal to θ plus a random error component, the distributions of which are known but need not be either iid nor normally distributed. Under these assumptions, the marginal likelihood of response \underline{x}_i obtained from population k is given as

$$h(\underline{x}_i | \Gamma, \Sigma) = \prod_k \left[\int_{\theta} p(\underline{x}_i | \theta) g_k(\theta | \Gamma, \Sigma) d\theta \right]^{I_{ik}}. \quad (3.1)$$

For notational convenience, we write simply $h(\underline{x}_i)$ and $g_k(\theta)$ hereafter, the dependence on Γ and Σ implicit.

From (3.1), the log marginal likelihood of samples of \underline{x} of size N_k is given by

$$\begin{aligned} \log L^* &= \sum_i \log h(\underline{x}_i) \\ &= \sum_i \sum_k I_{ik} \log \int_{\theta} p(\underline{x}_i | \theta) g_k(\theta) d\theta. \end{aligned} \quad (3.2)$$

The derivative of $\log L^*$ with respect to $\tilde{\Gamma}$ is then obtained as

$$\begin{aligned}\frac{\partial \log L^*}{\partial \tilde{\Gamma}} &= \sum_i \frac{\partial \log h(\tilde{x}_i)}{\partial \tilde{\Gamma}} \\ &= \sum_i \sum_k I_{ik} h^{-1}(\tilde{x}_i) \int_{\theta} p(\tilde{x}_i | \tilde{\theta}) \frac{\partial g_k(\tilde{\theta})}{\partial \tilde{\Gamma}} d\tilde{\theta} \\ &= \sum_i \sum_k I_{ik} h^{-1}(\tilde{x}_i) \int_{\theta} p(\tilde{x}_i | \tilde{\theta}) g_k(\tilde{\theta}) \tilde{\theta}^{-1} (\tilde{\theta} - \tilde{\Gamma}' \tilde{t}_k) \tilde{t}_k' d\tilde{\theta} . \quad (3.3)\end{aligned}$$

Equating to zero yields

$$\begin{aligned}&\sum_i \sum_k I_{ik} h^{-1}(\tilde{x}_i) \int_{\theta} p(\tilde{x}_i | \tilde{\theta}) g_k(\tilde{\theta}) \tilde{\theta} d\tilde{\theta} \tilde{t}_k' \\ &= \sum_i \sum_k I_{ik} h^{-1}(\tilde{x}_i) \int_{\theta} p(\tilde{x}_i | \tilde{\theta}) g_k(\tilde{\theta}) d\tilde{\theta} \tilde{\Gamma}' \tilde{t}_k \tilde{t}_k' ,\end{aligned}$$

then

$$\sum_k N_k \hat{\mu}_k^* \tilde{t}_k' = \sum_k N_k \tilde{\Gamma}' \tilde{t}_k \tilde{t}_k' , \quad (3.4)$$

where

$$\hat{\mu}_k^* = \int_{\tilde{\theta}} p_k(\tilde{\theta} | \tilde{x}) d\tilde{\theta} \quad (3.5)$$

with

$$\begin{aligned}p_k(\tilde{\theta} | \tilde{x}) &= N_k^{-1} \sum_i I_{ik} p(\tilde{\theta} | \tilde{x}_i) \\ &= N_k^{-1} \sum_i I_{ik} h^{-1}(\tilde{x}_i) p(\tilde{x}_i | \tilde{\theta}) g_k(\tilde{\theta}) \quad (3.6)\end{aligned}$$

being the posterior density of $\tilde{\theta}$ in population k given $\tilde{\Gamma}$, \tilde{x} , and the observed data (\tilde{x}) via Bayes theorem. Rewriting (3.4) more compactly,

$$\tilde{T}' \hat{D}M^* = \tilde{T}' \hat{D}T \tilde{\Gamma} ,$$

from which

$$\hat{\Sigma} = (\underline{T}' \underline{D} \underline{T})^{-1} \underline{T}' \hat{\underline{M}}^* . \quad (3.7)$$

Similarly, differentiating (3.2) with respect to $\underline{\Sigma}$ yields

$$\begin{aligned} \frac{\partial \log L^*}{\partial \underline{\Sigma}} &= \sum_i \frac{\partial \log h(\underline{x}_i)}{\partial \underline{\Sigma}} \\ &= \sum_i \sum_k I_{ik} \left\{ -\frac{1}{2} (2 \underline{\Sigma}^{-1} - \text{diag } \underline{\Sigma}^{-1}) + \frac{1}{2} h^{-1}(\underline{x}_i) \int_{\theta} p(\underline{x}_i | \theta) g_k(\theta) \right. \\ &\quad \times \left. \left[2 \underline{\Sigma}^{-1} (\underline{\theta} - \underline{\Gamma}' \underline{t}_k) (\underline{\theta} - \underline{\Gamma}' \underline{t}_k)' \underline{\Sigma}^{-1} \right. \right. \\ &\quad \left. \left. - \text{diag} [\underline{\Sigma}^{-1} (\underline{\theta} - \underline{\Gamma}' \underline{t}_k) (\underline{\theta} - \underline{\Gamma}' \underline{t}_k)' \underline{\Sigma}^{-1}] d\underline{\theta} \right] \right\} . \end{aligned} \quad (3.8)$$

Equating to zero then simplifying leads to

$$\text{diag } \underline{\Sigma} - 2 \underline{\Sigma} = \text{diag } \underline{S}^* - 2 \underline{S}^* ,$$

where

$$\underline{S}^* = \sum_k \int_{\theta} (\underline{\theta} - \underline{\Gamma}' \underline{t}_k) (\underline{\theta} - \underline{\Gamma}' \underline{t}_k)' p_k(\underline{\theta} | \underline{x}_i) d\underline{\theta} . \quad (3.9)$$

Again it is clear that

$$\hat{\underline{\Sigma}} = \underline{S}^* .$$

Like (2.3) and (2.6), (3.5) and (3.9) are standard formulas for computing means and dispersions from an approximation of an unknown density. Now the approximation is not based on a discrete set of sample points from the distribution but on an average over observations of the posterior density of $\underline{\theta}$ given each observation. These posterior densities, however, are computed via Bayes theorem in (3.6) with the true densities assumed known. Thus, the likelihood equations (3.7) and (3.10) constitute a system of implicit equations in $\underline{\Gamma}$ and $\underline{\Sigma}$, since they are defined in terms of $\hat{\underline{M}}^*$ and \underline{S}^* which depend in turn on $\underline{\Gamma}$ and $\underline{\Sigma}$ through h and g_k .

One approach to solving (3.7) and (3.10), thereby obtaining zeros of the log likelihood, is the so-called method of successive approximations.

That is, \hat{M}^* and \hat{S}^* are computed through (3.5) and (3.9) with provisional estimates $\hat{\Gamma}^t$ and $\hat{\Sigma}^t$; improved estimates $\hat{\Gamma}^{t+1}$ and $\hat{\Sigma}^{t+1}$ are then obtained by evaluating (3.7) and (3.10) with respect to these new values. This procedure will be recognized as an application of the EM algorithm, as described by Dempster, Laird, and Rubin (1977), who demonstrated convergence to a maximum of the likelihood function when the complete data density is a member of the exponential family, as it is in the problem at hand. The notoriously slow convergence of the EM algorithm, which worsens as the densities $p(\mathbf{x}|\boldsymbol{\theta})$ become more diffuse, can be largely ameliorated by the use of acceleration techniques such as those described by Ramsey (1975).

4. COMPUTING APPROXIMATIONS

Because closed-form expressions for the integrals in (3.1), (3.5), and (3.9) are not generally available, numerical approximations are required in applying the foregoing solution. Three approaches are outlined in this section: Gauss-Hermite quadrature, quadrature over fixed points, and Monte Carlo integration.

For accuracy and stability, Gauss-Hermite quadrature is the preferred method of numerical integration over the normal distribution when p is small. Stroud and Sechrist (1966) provide tables of optimal points and weights for the univariate standard normal density, which will be denoted (z_q) and $(W(z_q))$, for $q = 1, \dots, Q$. A grid of points for the p -variate standard normal is obtained as the Cartesian product of p univariate sets of points, with weights equal to the products of weights associated with each element in the vector defining a grid point. That is, a typical point in the

grid will take the form

$$\tilde{z}'_q = (z_{q1}, \dots, z_{qp})$$

and have an associated weight of

$$w(\tilde{z}_q) = \prod_{t=1}^p w(z_{qt}) .$$

The integrations in (3.1), (3.5), and (3.9) take place over a general p-variate normal distribution, necessitating a change of variables of integration in order for Gauss-Hermite quadrature to be employed. We illustrate with (3.1). Let $\tilde{z}_k = (\theta - \Gamma' \tilde{z}_k) v$, where $VV' = \Sigma$ is the Cholesky factorization of Σ (implying that $|v| = |\Sigma|^{1/2}$). Then

$$\begin{aligned} h(x_i) &= \prod_k \left\{ \int_{\theta} p(x_i | \theta) \frac{|\Sigma|^{-1/2}}{(2\pi)^{p/2}} \exp[-\frac{1}{2}(\theta - \Gamma' \tilde{z}_k)' \Sigma^{-1}(\theta - \Gamma' \tilde{z}_k)] d\theta \right\} I_{ik} \\ &= \prod_k \left\{ \int_{\tilde{z}_k} p(x_i | \theta_k(z_k)) \frac{|\Sigma|^{-1/2}}{(2\pi)^{p/2}} \exp(-\tilde{z}_k' z_k / 2) |v| dz_k \right\} I_{ik} \\ &= \prod_k \left\{ \int_{\tilde{z}_k} p(x_i | \theta_k(z_k)) (2\pi)^{-p/2} \exp(-\tilde{z}_k' z_k / 2) dz_k \right\} I_{ik} \end{aligned}$$

where

$$\theta_k(z) = Vz + \Gamma' \tilde{z}_k .$$

Then

$$h(x_i) \approx \prod_k \left\{ \sum_q p(x_i | x_{qk}) w(x_{qk}) \right\} I_{ik}$$

where

$$x_{qk} = \theta_k(z_q) \text{ and } w(x_{qk}) = w(z_q) .$$

Computing approximations of $\hat{\mu}_k^*$ and \hat{s}^* are obtained similarly as

$$\hat{\mu}_k^* \approx N_k^{-1} \sum_i I_{ik} h^{-1}(x_i) \sum_q x_{qk} p(x_i | x_{qk}) w(x_{qk}) = \sum_q x_{qk} p_{qk}^* \quad (4.1)$$

where

$$p_{qk}^* = N_K^{-1} \sum_i I_{ik} h^{-1}(x_i) p(x_i | x_{qk}) w(x_{qk})$$

and

$$\Sigma^* = \sum_k \sum_q (x_{qk} - \bar{x}_k)(x_{qk} - \bar{x}_k)' p_{qk}^* \quad (4.2)$$

The similarity of the computing approximations (4.1) and (4.2) to the complete data solution given as (2.3) and (2.6) are immediately apparent; means and dispersions are again computed with respect to a discrete approximation of the distribution of interest. This time, however, the discrete approximation is based not on sample points from that distribution but on posterior estimates of its density at selected quadrature points, given the observed data (\underline{x}). In contrast to (2.3) and (2.6), (4.1) and (4.2) constitute a system of implicit equations because of the dependence of the weights p_{qk}^* on the unknown parameters of the distribution.

An alternative approximation that can offer considerable computational advantage is quadrature over a fixed grid of points. Whereas Gauss-Hermite quadrature computes points anew each cycle in accordance with provisional estimates of Σ and Γ , it is possible to retain the same grid of points for all cycles and thereby avoid computing $p(x | x_{qk})$ every cycle. A grid of points x_q is selected a priori to span a region where the preponderance of the population distributions is believed to lie. New weights are computed in each cycle from provisional estimates of Σ and Γ as follows:

$$w_k(x_q) = \exp[-\frac{1}{2}(x_q - \bar{x}_k)' \Sigma^{-1}(x_q - \bar{x}_k)] .$$

The computing approximations (4.1) and (4.2) remain unchanged except for the substitutions of x_q for x_{qk} and $w_k(x_q)$ for $w(x_{qk})$. When the grid is well chosen, estimates of Σ and Γ will agree well with those computed via

Gauss-Hermite quadrature. When the points are poorly chosen, however, loss of accuracy and/or stability can result.

A second alternative that can prove useful when large p renders quadrature over a grid cumbersome is Monte Carlo integration. In each cycle, Q random points \tilde{x}_{qk} are generated for each population k in accordance with provisional estimates of $\tilde{\Gamma}$ and $\tilde{\Sigma}$. The computing formulas (4.1) and (4.2) remain unchanged except that

$$w(\tilde{x}_{qk}) = 1/Q \quad k = 1, \dots, K .$$

5. ASYMPTOTIC STANDARD ERRORS

Following Bock and Lieberman (1970), we may approximate the inverse of the asymptotic covariance matrix of the estimators $\hat{\Gamma}$ and $\hat{\Sigma}$ by

$$\hat{H} = \sum_i \left[\frac{\partial \log h(\tilde{x}_i)}{\partial \xi} \Bigg|_{\tilde{\xi}} \right] \left[\frac{\partial \log h(\tilde{x}_i)}{\partial \xi'} \Bigg|_{\tilde{\xi}} \right] ,$$

where ξ represents the M_p elements of $\tilde{\Gamma}$ and the $p(p+1)/2$ nonredundant elements of $\tilde{\Sigma}$ written as a single vector. Large sample standard errors are obtained as the square roots of the diagonal elements of \hat{H}^{-1} . Expressions necessary for the evaluation of \hat{H} are found in (3.3) and (3.8). Using the univariate case as an illustration, the required gradient vectors, gramian products of which are summed over observations to produce \hat{H} , are shown below:

$$\begin{aligned} \frac{\partial \log h(\tilde{x}_i)}{\partial \gamma_m} &= \sum_k I_{ik} h^{-1}(\tilde{x}_i) \int \theta p(\tilde{x}_i | \theta) \sigma^{-2} (\theta - \tilde{\Gamma}' \tilde{\xi}_k) t_{km} d\theta \\ &= \sigma^{-2} \sum_k I_{ik} h^{-1}(\tilde{x}_i) \sum_k p(\tilde{x}_i | \tilde{x}_{qk}) w(\tilde{x}_{qk}) (\tilde{x}_{qk} - \tilde{\Gamma}' \tilde{\xi}_k) t_{km} \\ &= \sigma^{-2} \sum_k I_{ik} \sum_q p(\tilde{x}_{qk} | \tilde{x}_i) (\tilde{x}_{qk} - \tilde{\Gamma}' \tilde{\xi}_k) t_{km} \end{aligned}$$

and

$$\begin{aligned}\frac{\partial \log h(\tilde{x}_i)}{\partial \sigma^2} &= -\frac{1}{2\sigma^2} + \frac{1}{2\sigma^4} \sum_k I_{ik} h^{-1}(\tilde{x}_i) \int \theta p(x_i | \theta) g_k(\theta) (\theta - \tilde{t}_k)(\theta - \tilde{t}_k)' d\theta \\ &\approx -\frac{1}{2\sigma^2} + \frac{1}{2\sigma^4} \sum_k I_{ik} \sum_q p(x_{qk} | \tilde{x}_i) (x_{qk} - \tilde{t}_k)(x_{qk} - \tilde{t}_k)' .\end{aligned}$$

6. TESTS OF FIT

Consider two competing models for a given data set, with Model 1 nested within Model 2. In large samples, the fit of the two models can be compared by means of the statistic

$$\chi^2 = -2 \log(L_1^*/L_2^*) \quad (6.1)$$

which, when Model 1 is correct, follows a chi-square distribution with degrees of freedom equal to the number of additional parameters in Model 2.

When the number of potential responses \tilde{x} is small compared to the sample size, it is possible to compare the fit of a given model to a general multinomial alternative. First the universe of potential responses \tilde{x}_l is partitioned into mutually exclusive and exhaustive classes such that the potential responses of a given observation constitute exactly one class. If a test with several parallel forms is administered, for example, each class of responses will consist of all possible response vectors to the items in a given test form. Let $r(\tilde{x}_{lk})$ be the count of response \tilde{x}_l observed in population k , and let $N(\tilde{x}_{lk})$ be the total number of responses from the same class as \tilde{x}_l that are observed in population k . Then the statistic

$$\chi^2 = -2 \sum_l \sum_k r(\tilde{x}_{lk}) \log(N(\tilde{x}_{lk})h(\tilde{x}_{lk})/r(\tilde{x}_{lk})) \quad (6.2)$$

[with terms for which $r(\tilde{x}_{ik}) = 0$ set to zero] will follow a chi-square distribution in large samples when the model is correct, with degrees of freedom equal to the number of non-zero $r(\tilde{x}_{ik})$ terms minus the number of parameters estimated in the model minus K . It will be noted that the difference between the values of (6.2) for two nested models takes the same value and has the same degrees of freedom as a direct comparison via (6.1).

Following Andersen (1980), we may test the equality of dispersion matrices across groups in a two-step procedure. First, means and dispersion matrices are estimated in all groups separately. The product of the likelihoods resulting from these separate analyses is accumulated. Second, separate means and a common dispersion matrix are estimated by employing an identity matrix as the basis matrix \mathbf{T} and proceeding as described in Section 3. The resulting likelihood may be compared with the first via (6.2) to obtain a large-sample chi-square test of the equality of dispersion matrices over groups, with the number of degrees of freedom equal to $(K - 1)p(p + 1)/2$.

7. A NUMERICAL EXAMPLE

Item response models in psychometrics express the probability of a given response to a test item as a function of a subject's latent ability parameter θ and one or more parameters that characterize the regression of the item response on ability. The three-parameter logistic item response model (Birnbaum, 1968) for dichotomous items, for example, gives the probability of a correct response to item j from subject i as

$$\begin{aligned} P(x_{ij} = 1 | \theta_i, a_j, b_j, c_j) \\ = p_{ij} \\ = c_j + (1 - c_j) \frac{\exp[1.7a_j(\theta_i - b_j)]}{1 - \exp[1.7a_j(\theta_i - b_j)]}, \end{aligned} \quad (7.1a)$$

and the probability of an incorrect response as

$$P(x_{ij} = 0 | \theta_i, a_j, b_j, c_j) = 1 - P_{ij}, \quad (7.1b)$$

where x_{ij} denotes the response, 1 if correct and 0 if not, and where θ_i is the ability of subject i and a_j , b_j , and c_j are parameters that characterize item j : a_j , the slope parameter, reflects the reliability of the item; b_j , the threshold, reflects its difficulty; and c_j , the lower asymptote, reflects the minimal probability of a correct response from even subjects with extremely low abilities. Under the usual assumption of local or conditional independence, the probability of a pattern of responses from subject i to a number of items is given by the product over items of expression like (7.1):

$$P(\tilde{x}_i | \theta) = \prod_j P(x_{ij} | \theta_i, a_j, b_j, c_j). \quad (7.2)$$

In most applications, item response models are used to estimate the latent abilities of individuals. With values of item parameters assumed known (generally estimated from a large sample of subjects), one may obtain a maximum likelihood estimate of θ with respect to a given response vector by maximizing (7.2) as a function of θ , and a large-sample standard error by taking the negative reciprocal of the second derivative of the natural logarithm of (7.2) evaluated at the mle $\hat{\theta}$.

There are several reasons not to approximate the distribution of θ in a population from the distribution of $\hat{\theta}$, or to carry out ANOVA procedures on values of $\hat{\theta}$ to estimate group effects on means of θ in various subpopulations. First, values of θ are estimated with varying precision, thereby violating the assumptions upon which standard ANOVA procedures are based. Second, estimation of θ from certain response patterns is problematic; patterns with all correct or all incorrect responses, along with most patterns

with total scores below chance level (the sum of the c_j 's over the items a subject has been presented) yield infinite mle's. Deleting the data of subjects with such patterns biases estimates of the population means and variances, while assigning them finite values either arbitrarily or by incorporating prior information introduces biases into the estimation of the θ 's themselves. Third, stable estimation of individuals' θ 's requires at least 15 or 20 responses per subject, thereby proscribing the use of more efficient sampling designs that would be preferred when only population-level parameters are of interest. The methods introduced in the preceding sections suffer none of these deficiencies.

As an example, we consider data from the Profile of American Youth, a survey of the aptitudes of a sample of the population of Americans aged 16 through 23 in July 1980 (U.S. Department of Defense, 1982). Table 1 presents counts of the sixteen possible response patterns observed to four items from the Arithmetic Reasoning test of the Armed Services Vocational Aptitude Battery (ASVAB), Form 8A, as observed in samples of white males and females and black males and females. The parameters of these items under the three-parameter logistic item response model, shown in Table 2, were estimated from a sample of 1,178 cases from the 11,787 available using the BILOG computer program (Mislevy and Bock, 1982).

Tables 3 and 4 presents the results of fitting a series of nested models to the data of Table 1. Examination of the differences between likelihood ratio chi-squares against the general multinomial alternative suggests, to begin with, that within-group variation may not be homogeneous. Continuing the example for purposes of illustration, we find strong evidence for a race effect and, to a lesser extent, for sex and interaction effects.

The males' mean exceeds that of the females for whites, but the females' mean appears to equal or exceed that of the males for blacks.

INSERT TABLES 1-4

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TABLE 1
COUNTS OF OBSERVED RESPONSE PATTERNS

| ITEM RESPONSE | | | | WHITE MALES | WHITE FEMALES | BLACK MALES | BLACK FEMALES |
|------------------|---|---|---|----------------|------------------|----------------|------------------|
| 1 | 2 | 3 | 4 | | | | |
| 0 | 0 | 0 | 0 | 23 | 20 | 27 | 29 |
| 0 | 0 | 0 | 1 | 5 | 8 | 5 | 8 |
| 0 | 0 | 1 | 0 | 12 | 14 | 15 | 7 |
| 0 | 0 | 1 | 1 | 2 | 2 | 3 | 3 |
| 0 | 1 | 0 | 0 | 16 | 20 | 16 | 14 |
| 0 | 1 | 0 | 1 | 3 | 5 | 5 | 5 |
| 0 | 1 | 1 | 0 | 6 | 11 | 4 | 6 |
| 0 | 1 | 1 | 1 | 1 | 7 | 3 | 0 |
| 1 | 0 | 0 | 0 | 22 | 23 | 15 | 14 |
| 1 | 0 | 0 | 1 | 6 | 7 | 10 | 10 |
| 1 | 0 | 1 | 1 | 19 | 6 | 1 | 2 |
| 1 | 1 | 0 | 0 | 21 | 18 | 7 | 19 |
| 1 | 1 | 0 | 1 | 11 | 15 | 9 | 5 |
| 1 | 1 | 1 | 0 | 23 | 20 | 10 | 8 |
| 1 | 1 | 1 | 1 | 86 | 42 | 2 | 4 |
| TOTAL | | | | 264 | 227 | 141 | 147 |

TABLE 2
ITEM PARAMETERS

| ITEM | a | b | c |
|------|------|------|-----|
| 1 | 1.27 | -.13 | .22 |
| 2 | 1.45 | .42 | .34 |
| 3 | 2.49 | .71 | .31 |
| 4 | 2.27 | .62 | .20 |

TABLE 3
PARAMETER ESTIMATES AND FIT STATISTICS

| EFFECTS IN MODEL | MEAN | RACE | SEX | INTERACTION | VARIANCE | CHI-SQUARE | DF |
|---|------------|-----------|-----------------------------------|-------------|-----------|------------|----|
| GRAND MEAN | .02 (.05) | -- | -- | -- | .85 (.12) | 223.77 | 57 |
| GRAND MEAN, SEX | .02 (.05) | -- | .29 (.09) | -- | .83 (.12) | 213.31 | 56 |
| GRAND MEAN, RACE | -.11 (.06) | .92 (.11) | -- | -- | .66 (.11) | 124.14 | 56 |
| GRAND MEAN, RACE, SEX, | -.11 (.06) | .91 (.11) | .24 (.09) | -- | .65 (.10) | 115.92 | 55 |
| GRAND MEAN, RACE, SEX, INTERACTION | -.11 (.06) | .90 (.11) | .13 (.11) | .42 (.21) | .65 (.10) | 111.12 | 54 |
| UNCONSTRAINED MEANS, UNCONSTRAINED VARIANCES | | | (VARIANCES = 1.06, .63, .39, .27) | | | 100.57 | 51 |

TABLE 4
FITTED MEANS

| EFFECTS IN MODEL | WHITE MALES | WHITE FEMALES | BLACK MALES | BLACK FEMALES |
|--|----------------|------------------|----------------|------------------|
| GRAND MEAN | .02 | .02 | .02 | .02 |
| GRAND MEAN, SEX | .16 | -.13 | .16 | -.13 |
| GRAND MEAN, RACE | .35 | .35 | -.57 | -.57 |
| GRAND MEAN, RACE, SEX | .47 | .22 | -.44 | -.69 |
| GRAND MEAN, RACE, SEX, INTERACTION | .51 | .16 | -.60 | -.52 |
| UNCONSTRAINED MEANS, UNCONSTRAINED VARIANCES | .49 | .17 | -.46 | -.37 |

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